

*****	24	94	17.5	450	1	W46506	Tyrosine kinase associ	7.31e+00
*****	25	93	17.3	740	1	W68338	Plasmodium falciparum	8.60e+00
*****	26	93	17.3	740	1	R2530	Plasmodium falciparum	8.60e+00
*****	27	92	17.1	432	1	W9354	Human regulatory molec	1.10e+01
*****	27	91	16.9	265	1	W9271	Human regulatory molec	1.10e+01
*****	28	91	16.9	521	1	W77802	Human secreted protein	1.19e+01
*****	29	91	16.9	541	1	W37148	Mammalian Era (Mena).	1.19e+01
*****	30	91	16.9	783	1	W37151	Mouse neural Men++ pro	1.19e+01
*****	31	91	16.9	787	1	W37152	Mouse neural Men++ pr	1.19e+01
*****	32	91	16.9	802	1	W37153	Mouse neural Men++ p	1.19e+01
*****	33	91	16.9	83	1	R0428	Arp 4.	1.40e+01
*****	34	90	16.7	386	1	R05849	Protein Arp 4.	1.40e+01
*****	35	90	16.7	301	1	P70867	Sequence of acidic bas	1.64e+01
*****	36	89	16.5	433	1	W03389	Mouse SH3P7 protein.	1.64e+01
*****	37	89	16.5	1088	1	W17786	Human multiple regulat	1.64e+01
*****	38	89	16.5	1382	1	W31867	Human metastasis assoc	1.93e+01
*****	39	88	16.4	83	1	R90346	PUG4-5-CDKBP clone de	2.26e+01
*****	40	87	16.2	86	1	W95073	GST-HD fusion protein	2.26e+01
*****	41	87	16.2	86	1	W95078	GST-HD fusion protein	2.26e+01
*****	42	87	16.2	94	1	W95580	GST-HD fusion protein	2.26e+01
*****	43	87	16.2	94	1	W95075	GST-HD fusion protein	2.26e+01
*****	44	87	16.2	94	1	W95077	Hordeum vulgare antim	2.26e+01
*****	45	87	16.2	637	1	W62837	ALIGNMENTS	
Title:	>US-09-331-631-3							
Description:	- {117-185} from US09331631.PEP (4 of 5)							
Perfect Score:	538							
Sequence:	1 NRQDPQQYQOCQERCQH... EEQQREDEBEKYEERMKEEDN 69							
Scoring table:	PAM 150							
Searched:	Gap 11 188963 seqs., 23686106 residues							
Post-processing:	Minimum Match 0% summaries							
Database:	a-geneseq35 1:geneseq							
Statistics:	Mean 25.025; Variance 122.724; scale 0.204							
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES								
Result No.	Score	Query Length	DB ID	Description	Pred. No.	RESULT	1	
1	538	100.0	666	1 W62829	W62829	standard; Protein; 666 AA.	ID	
2	517	96.1	666	1 W62828	R22829;	(first entry)	AC	
3	512	95.2	625	1 W62830	Macadamia integrifolia	antimicrobial protein; infestation; control.	CC	
4	490	95.0	525	1 W62831	Macadamia integrifolia	antimicrobial protein; infestation; control.	OS	
4	220	40.9	525	1 R02081	Theobroma cacao antimi	antimicrobial protein; infestation; control.	KW	
6	204	37.9	590	1 W62832	Sequence encoded by Gossypium hirsutum ant	antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals.	CC	
7	130	24.2	524	1 W90340	G. max truncated SBP1	1.46e-09	CC	
8	130	24.2	524	1 W90339	G. max SBP1 protein.	1.46e-09	CC	
9	115	21.4	593	1 W62835	Zea mays antimicrobial	1.46e-09	CC	
10	110	20.4	28	1 W62841	Stenocarpus sinuatus a	1.46e-09	CC	
11	107	19.9	33	1 W62836	Zea mays antimicrobial	2.81e-08	CC	
12	107	19.9	303	1 R60054	Dirofilaria immitis pa	2.81e-08	CC	
13	107	19.9	409	1 W90342	G. max truncated SBP2	1.68e-02	CC	
14	107	19.9	489	1 W90341	G. max SBP2 protein.	1.68e-02	CC	
15	104	19.3	395	1 W03474	Mouse SRY-related prot	2.21e-01	CC	
16	104	18.2	35	1 R21079	Antimicrobial maize pe	5.16e-01	CC	
17	98	1562	1 R70491	Leucocytozoan protozoa	3.80e+00	CC		
18	98	1752	1 Y07031	Breast cancer associa	3.80e+00	CC		
19	97	18.0	316	1 R26941	P.falciparum LISA-R-NR	4.48e+00	CC	
20	97	18.0	482	1 Y07067	Renal cancer associate	4.48e+00	CC	
21	97	18.0	493	1 R26944	P.falciparum LSA gene	4.48e+00	CC	
22	97	17.5	175	1 W26536	Tripanosoma cruzi anti	7.31e+00	CC	
23	94	17.5	265	1 R12844	HTLV-1 protein express	7.31e+00	CC	



Qy 119 QDPQQQEQQCERQRHETPRHMTCQQRERRYEKEKRKQQKRYEEQQREDEEKEYEE 178  
 ID W62832 standard; Protein: 590 AA.  
 AC | | ;  
 DT 27-OCT-1998 (first entry)  
 DE Gossypium hirsutum antimicrobial protein.  
 KW antimicrobial protein; infestation; control.  
 OS Gossypium hirsutum.  
 PN WO927905-A1.

PD 02-JUL-1998.

PF 22-DEC-1997; AU0874.

PR 20-DEC-1996; AU004275.

PA (RETR.) COOP RES CENT TROPICAL PLANT PATHOLOGY.

PI Bower NI, Goulier RC, Green JL, Manners JM, Marcus JP;

DR WPI; 98-377279/32.

Novel anti-microbial protein from e.g. Macadamia integrifolia - useful for controlling microbial infestations of plants or mammals

PT PS Claim 1; Page 49-51; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals.

CC Sequence 590 AA;

SQ

CC seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.

CC Sequence 444 AA;

RESULT 6 Query Match 24.2%; Score 130; DB 1; Length 444;  
 ID W62832 standard; Protein: 590 AA.  
 AC | | ;  
 DT 27-OCT-1998 (first entry)  
 DE G. max SBP1 protein.

KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean; Glycine max.

OS WO927905-A1.

PN 26-NOV-1998.

PF 21-MAY-1998; AU0465.

PR 22-MAY-1997; US-1998-047558.

PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.

PI Chao WS, Grimes HD;

DR WPI; 99-070155-06.

PT New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds

PS Disclosure; Page 34-36; 58pp; English.

Db 78 HRPEPDPPRYYEQCQEQ-RQQE-B-RQPOCQCRKLRKFEQEQQOSQRQFQEQCQHQQE 135  
 Qy 117 NRQRDPOQQYEQQCERQRHETPRHMTCQQRERRYEKEKRKQQKRYEE-QQR-EDEE 174  
 ID 136 QRPEKKQQ 143  
 PT Qy 175 KVEERMKE 182

RESULT 7 Query Match

Best Local Similarity 38.2%; Pred. No. 2.81e-08; Length 590:  
 ID W90340 standard; protein: 444 AA.

AC W90340; 26; Conservative 21; Mismatches 17; Indels 4; Gaps 4;

DT 24-MAY-1999 (first entry)

DE G. max truncated SBP1 protein.

DB 117 NRQRDPOQQYEQQCERQRHETPRHMTCQQRERRYEKEKRKQQKRYEE-QQR-EDEE 174

Qy 175 KVEERMKE 182

RESULT 8 Query Match

Best Local Similarity 37.9%; Score 204; DB 1; Length 590:  
 ID W90339 standard; protein: 524 AA.

AC W90339; 26; Conservative 21; Mismatches 17; Indels 4; Gaps 4;

DT 24-MAY-1999 (first entry)

DE G. max SBP1 protein.

DB 43 CRHQCQQQQYTEGDKRVCQSCDR-YHRMKQEREKOIETTREKE-ESREREE 97  
 Qy 129 CQERCORHETPR-HMQTCQQRERRYEKEKRKQQKRYEE-QOREDEEKEYEERMKEED 184

RESULT 9 Query Match

Best Local Similarity 31.6%; Pred. No. 1.68e-02; Length 524:  
 ID W62835 standard; Protein: 593 AA.

AC W62835; 18; Conservative 16; Mismatches 20; Indels 3; Gaps 3;

DT 27-OCT-1998 (first entry)

DE Zea mays antimicrobial protein; infestation; control.

KW Zea mays antimicrobial protein; infestation; control.

OS Zea mays.

PN WO927905-A1.

PR 02-JUL-1998.

PF 22-DEC-1997; AU0874.

PR 20-DEC-1996; AU004275.

(RETR.) COOP RES CENT TROPICAL PLANT PATHOLOGY.

This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in





